

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANS  
GIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLS  
SEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCR  
GRLDKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHGPVNSELF  
LRHVPGWLRPLLRL  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARD  
DRAAHLWEASKRL  
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPOSSPD  
LSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

# FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
 GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
 CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCCAGAC  
 CCACACCACCTCCTGCCTGATGGGACCCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT  
 CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
 GCCCTCCAGCCCAGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC  
 CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT  
 CCTGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCGCAGAGCTTGGAGGCCCTCACTGGGGCCAAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGAAAAAGTGCCAGTGCCCCACCTCAGGAA  
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCACAAATGGCATC  
 ATCCGTGGCTACCAAGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACTGGACTGTAGTTGGTGAGCAG  
 ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCT  
 GGGGAGCCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAAGAACCCAGTGAGCAT  
 GGTCCCTGGACCTTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCAATTGCCACCTGCGGTGTTGCACTC  
 TGGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTGGGCCCAGGTCTG  
 TACAGATATACAGTGAGGATGCCATCCTAAAAACAGGATGGATCACAGTGAATCCCAGTGGTTGGCAGACACT  
 TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCCTCAGCAGTCCGGCTGGGGGCGGATGCCCGG  
 GACCCACTAGACTGTGCTGCTCCTTGTCTCTCGTGGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCAGTCCCAGCT  
 AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCAGTCCCAGCT  
 GTCAGGCGCTCCCAACCCAGCTGGCCAGCTCTCCAGCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCCGCAGG  
 GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGAAGGCCAAAAAGAGCAGGAGCTGCAGCAT  
 GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTC  
 AAGAACCCTTTCCCAAGCCAGGAGCTGTGCCCCAAGCTCTGGTTGCCCTGGCGGGCCCTGGGACCGAAACTCCTC  
 AGCTCCTCAAATGAGCTGGTTACTCGTCACTCTCCCTCAGCAGCCCTCTTCTCATGAAACTCCCCCAACTCAG  
 AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCAGTCCCCATC  
 CTTAGCCCTGCACTCCCCCTAGCCCCCAGGCTCTTCCCTCTCTGGCCCCCAGCCAGCTTCCAGTGCCTGTCC  
 AGCTCCTCACTGTCACTCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
 CTCAGTGAGGGTGAGGAGACTCCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT  
 GGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGGACTCCCGAAGGCTCCTTACCCCAATGGTTGGGGC  
 GGAGTCTTGTGTGCCCCACCTCGGCCCTGCCTCACCCCCACCCCGAGCGAGGGCTCCTTAGCCCAATGGTTGGGGC  
 TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCTCGCTGAT  
 GCTCACTTTGCCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTTCGGTCTAGAGCCAGGGAGGCAGACTGC  
 GTCTTCATAGATGCCTCATACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCTTG  
 TGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGCTGGGAAGGGGGATGCCTCCC  
 TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCAGCTCCACTGTCGTATGCCCAAGGCTGGTGCTTCTCCT  
 GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
 ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
 TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
 ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACAGGTTGTTTTGGC  
 CTGAGGAGCAGCCCTGCCTGCTGCTTCTCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT  
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT  
 GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG  
 AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
 TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT  
 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

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VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARA EKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPV ELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVA AVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPVAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANS SPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPV DYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753